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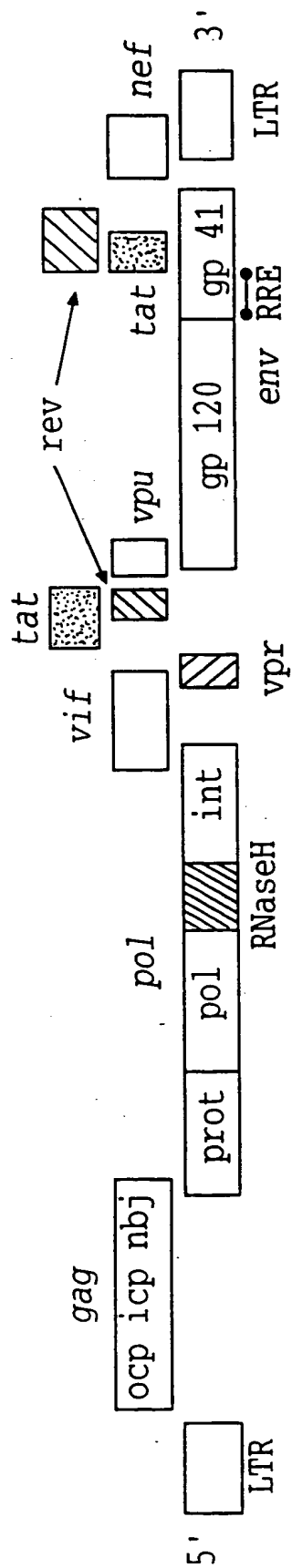
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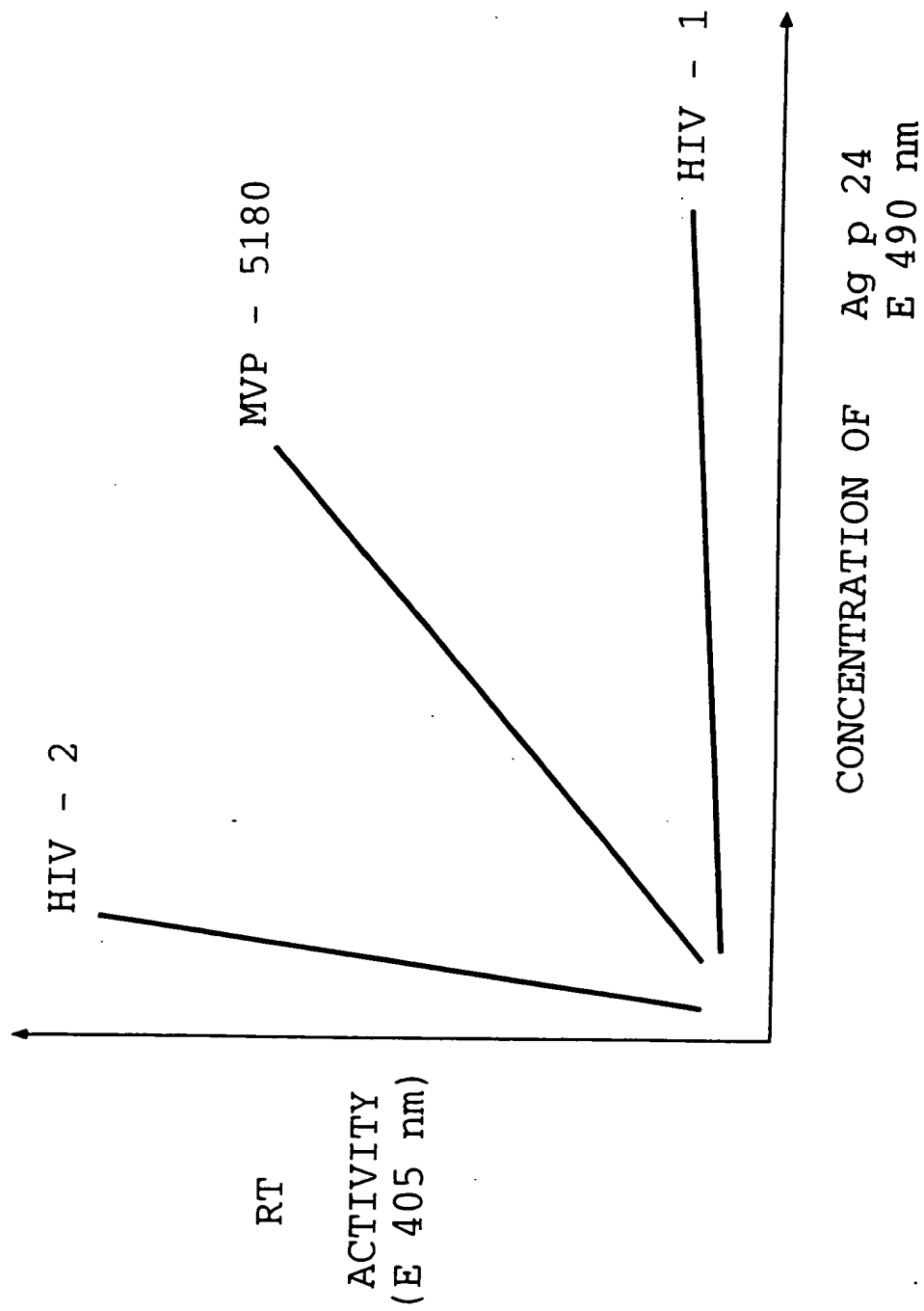
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FIG. 1



**FIG. 2**

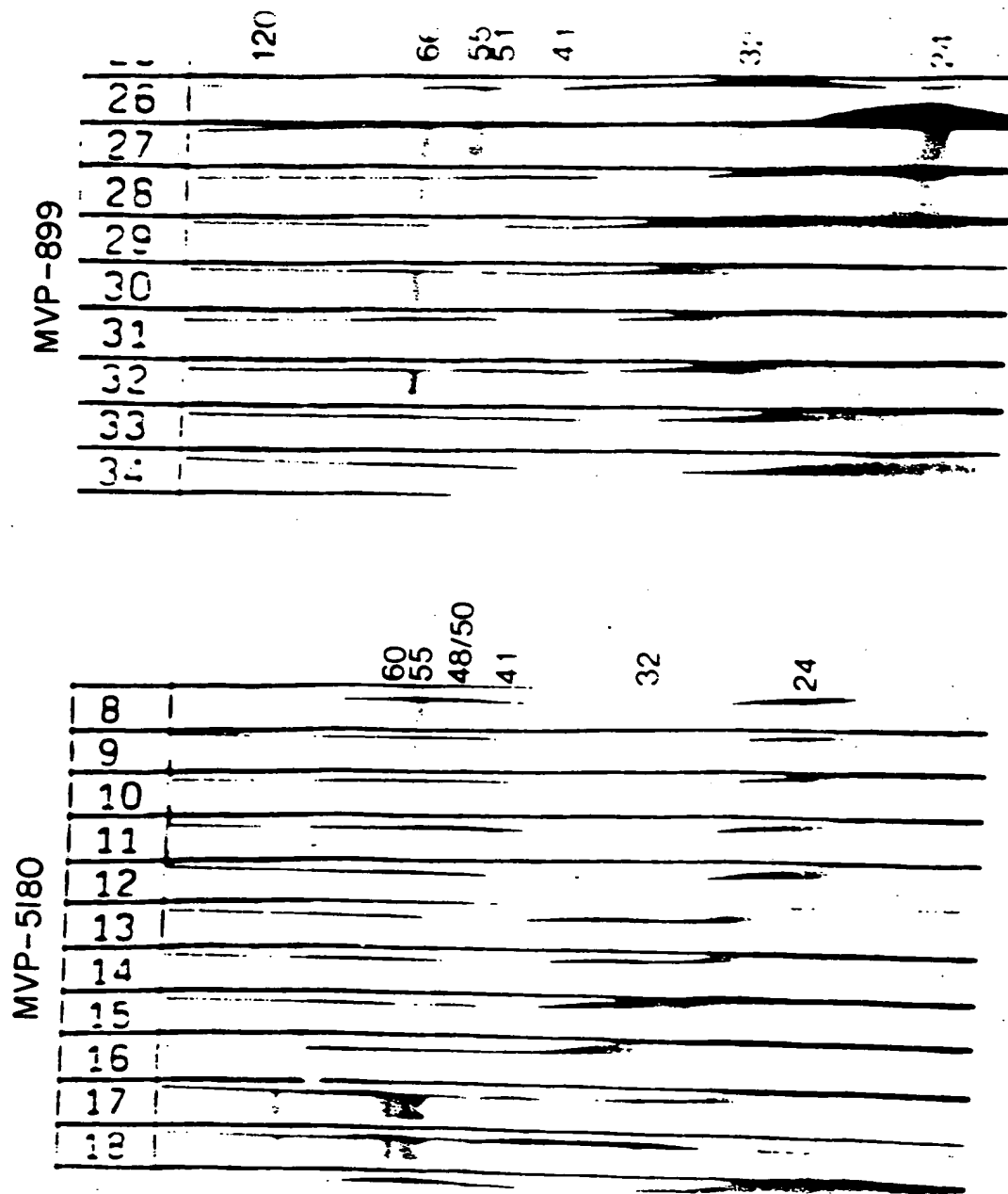


FIG. 3

SEQUENCE OF MVP-5180

(SEQ. ID NO. 56)

1 CTGGATGGGT TAATTTACTC CCATAAGAGA GCAGAAATCC TGGATCTCTG  
51 GATATATCAC ACTCAGGGAT TCTTCCCTGA TTGGCAGTGT TACACACCGG  
101 GACCAGGACC TAGATTCCCA CTGACATTTG GATGGTTGTT TAAACTGGTA  
151 CCAGTGTCAG CAGAAGAGGC AGAGAGACTG GGTAATACAA ATGAAGATGC  
201 TAGTCTTCTA CATCCAGCTT GTAATCATGG AGCTGAGGAT GCACACGGGG  
251 AGATACTAAA ATGGCAGTTT GATAGATCAT TAGGCTTAAC ACATATAGCC  
301 CTGCAAAAGC ACCCAGAGCT CTTCCCCAAG TAACTGACAC TGCGGGACTT  
351 TCCAGACTGC TGACACTGCG GGGACTTTCC AGCGTGGGAG GGATAAGGGG  
401 CGGTTCGGGG AGTGGCTAAC CCTCAGATGC TGCATATAAG CAGCTGCTTT  
451 CCGCTTGTAC CGGGTCTTAG TTAGAGGACC AGGTCTGAGC CCGGGAGCTC  
501 CCTGGCCTCT AGCTGAACCC GCTGCTTAAC GCTCAATAAA GCTTGCCCTG  
551 AGTGAGAAGC AGTGTGTGCT CATCTGTTCA ACCCTGGTGT CTAGAGATCC  
601 CTCAGATCAC TTAGACTGAA GCAGAAAATC TCTAGCAGTG GCGCCCGAAC  
651 AGGGACGCGA AAGTGAAAGT GGAACCAGGG AAGAAAACCT CCGACGCAAC  
701 GGGCTCGGCT TAGCGGAGTG CACCTGCTAA GAGGCGAGAG GAACTCACAA  
751 GAGGGTGAGT AAATTTGCTG GCGGTGGCCA GACCTAGGGG AAGGGCGAAG  
801 TCCCTAGGGG AGGAAGATGG GTGCGAGAGC GTCTGTGTTG ACAGGGAGTA  
851 AATTGGATGC ATGGGAACGA ATTAGGTTAA GGCCAGGATC TAAAAAGGCA  
901 TATAGGCTAA AACATTTAGT ATGGGCAAGC AGGGAGCTGG AAAGATACGC  
951 ATGTAATCCT GGTCTATTAG AAACCTGCAGA AGGTACTGAG CAACTGCTAC  
1001 AGCAGTTAGA GCCAGCTCTC AAGACAGGGT CAGAGGACCT GAAATCTCTC  
1051 TGGAACGCAA TAGCAGTACT CTGGTGCGTT CACAACAGAT TTGACATCCG  
1101 AGATACACAG CAGGCAATAC AAAAGTTAAA GGAAGTAATG GCAAGCAGGA  
1151 AGTCTGCAGA GGCCGCTAAG GAAGAAACAA GCCCTAGGCA GACAAGTCAA  
1201 AATTACCCTA TAGTAACAAA TGCACAGGGA CAAATGGTAC ATCAAGCCAT

**FIG. 4-1**

|      |            |            |            |            |            |
|------|------------|------------|------------|------------|------------|
| 1251 | CTCCCCCAGG | ACTTTAAATG | CATGGGTAAA | GGCAGTAGAA | GAGAAGGCCT |
| 1301 | TTAACCCTGA | AATTATTCCT | ATGTTTATGG | CATTATCAGA | AGGGGCTGTC |
| 1351 | CCCTATGATA | TCAATACCAT | GCTGAATGCC | ATAGGGGGAC | ACCAAGGGGC |
| 1401 | TTTACAAGTG | TTGAAGGAAG | TAATCAATGA | GGAAGCAGCA | GAATGGGATA |
| 1451 | GAACTCATCC | ACCAGCAATG | GGGCCGTTAC | CACCAGGGCA | GATAACGGAA |
| 1501 | CCAACAGGAA | GTGACATTGC | TGGAACAAC  | AGCACACAGC | AAGAGCAAAT |
| 1551 | TATATGGACT | ACTAGAGGGG | CTAACTCTAT | CCCAGTAGGA | GACATCTATA |
| 1601 | GAAAATGGAT | AGTGCTAGGA | CTAAACAAAA | TGGTAAAAAT | GTACAGTCCA |
| 1651 | GTGAGCATCT | TAGATATTAG | GCAGGGACCA | AAAGAACCAT | TCAGAGATTA |
| 1701 | TGTAGATCGG | TTTTACAAAA | CATTAAGAGC | TGAGCAAGCT | ACTCAAGAAG |
| 1751 | TAAAGAATTG | GATGACAGAA | ACCTTGCTTG | TTCAGAATTC | AAACCCAGAT |
| 1801 | TGTAAACAAA | TTCTGAAAGC | ATTAGGACCA | GAAGCTACTT | TAGAAGAAAT |
| 1851 | GATGGTAGCC | TGTCAAGGAG | TAGGAGGGCC | AACTCACAAG | GCAAAAATAC |
| 1901 | TAGCAGAAGC | AATGGCTTCT | GCCCAGCAAG | ATTTAAAAGG | AGGATACACA |
| 1951 | GCAGTATTCA | TGCAAAGAGG | GCAGAATCCA | AATAGAAAAG | GGCCCATAAA |
| 2001 | ATGCTTCAAT | TGTGGAAGAG | AGGGACATAT | AGCAAAAAC  | TGTCGAGCAC |
| 2051 | CTAGAAAAAG | GGGTGCTGG  | AAATGTGGAC | AGGAAGGTCA | CCAAATGAAA |
| 2101 | GATTGCAAAA | ATGGAAGACA | GGCAAATTTT | TTAGGGAAGT | ACTGGCCTCC |
| 2151 | GGGGGGCAGC | AGGCCAGGCA | ATTATGTGCA | GAAACAAGTG | TCCCCATCAG |
| 2201 | CCCCACCAAT | GGAGGAGGCA | GTGAAGGAAC | AAGAGAATCA | GAGTCAGAAG |
| 2251 | GGGGATCAGG | AAGAGCTGTA | CCCATTGTC  | TCCCTCAAAT | CCCTCTTTGG |
| 2301 | GACAGACCAA | TAGTCACAGC | AAAGGTTGGG | GGTCATCTAT | GTGAGGCTTT |
| 2351 | ACTGGATACA | GGGGCAGATG | ATACAGTATT | AAATAACATA | CAATTAGAAG |
| 2401 | GAAGATGGAC | ACCAAAAATG | ATAGGGGGTA | TAGGAGGCTT | TATAAAAGTA |
| 2451 | AAAGAGTATA | ACAATGTGAC | AGTAGAAGTA | CAAGGAAAGG | AAGTACAGGG |
| 2501 | AACAGTATTG | GTGGGACCTA | CTCCTGTAA  | TATTCTTGGG | AGAAACATAT |
| 2551 | TGACAGGATT | AGGATGTACA | CTAAATTTCC | CTATAAGTCC | CATAGCCCCA |

**FIG. 4-2**

2601 GTGCCAGTAA AGCTAAAACC AGGAATGGAT GGACCAAAG TAAACAATG  
 2651 GCCCCTATCT AGAGAGAAAA TAGAAGCACT AACTGCAATA TGTCAAGAAA  
 2701 TGGAACAGGA AGGAAAAATC TCAAGAATAG GACCTGAAAA TCCTTATAAT  
 2751 ACACCTATTT TTGCTATAAA AAAGAAAGAT AGCACTAAGT GGAGAAAATT  
 2801 GGTAGACTTC AGAGAATTAA ATAAAAGAAC ACAAGATTTC TGGGAGGTGC  
 2851 AATTAGGTAT TCCACATCCA GGGGGTTTAA AGCAAAGGCA ATCTGTTACA  
 2901 GTCTTAGATG TAGGAGATGC TTATTTCTCA TGCCCTTTAG ATCCAGACTT  
 2951 TAGAAAATAC ACTGCCTTCA CTATTCCTAG TGTGAACAAT GAGACCCAG  
 3001 GAGTAAGATA CCAGTACAAT GTCCTCCCGC AAGGGTGGAA AGG TTCACCA  
 3051 GCCATATTTC AGAGTTCAAT GACAAAGATT CTAGATCCAT TTAGAAAAG  
 3101 CAACCCAGAA GTAGAAATTT ATCAGTACAT AGATGACTTA TATGTAGGAT  
 3151 CAGATTTACC ATTGGCAGAA CATAGAAAGA GGGTCGAATT GCTTAGGGAA  
 3201 CATTTATATC AGTGGGGATT TACTACCCCT GATAAAAAGC ATCAGAAGGA  
 3251 ACCTCCCTTT TTATGGATGG GATATGAGCT CCACCCAGAC AAGTGGACAG  
 3301 TACAGCCCAT CCAATTGCCT GACAAAGAAG TGTGGACAGT AAATGATATA  
 3351 CAAAATTAG TAGGAAAATT AAATTGGGCA AGTCAAATCT ATCAAGGAAT  
 3401 TAGAGTAAAA GAATTGTGCA AGTTAATCAG AGGAACCAAA TCATTGACAG  
 3451 AGGTAGTACC TTTAAGTAAA GAGGCAGAAC TAGAATTAGA AGAAAACAGA  
 3501 GAAAAGCTAA AAGAGCCAGT ACATGGAGTA TATTACCAGC CTGACAAAGA  
 3551 CTTGTGGGTT AGTATTCAGA AGCATGGAGA AGGGCAATGG ACTTACCAGG  
 3601 TATATCAGGA TGAACATAAG AACCTTAAA CAGGAAAATA TGCTAGGCAA  
 3651 AAGGCCTCCC ACACAAATGA TATAAGACAA TTGGCAGAAG TAGTCCAGAA  
 3701 GGTGTCTCAA GAAGCTATAG TTATATGGGG GAAATTACCT AAATTCAGGC  
 3751 TGCCAGTTAC TAGAGAACT TGGGAACTT GGTGGGCAGA ATATTGGCAG  
 3801 GCCACCTGGA TTCCTGAATG GGAATTTGTC AGCACACCCC CATTGATCAA  
 3851 ATTATGGTAC CAGTTAGAAA CAGAACCTAT TGTAGGGGCA GAAACCTTTT  
 3901 ATGTAGATGG AGCAGCTAAT AGGAATACAA AACTAGGAAA GCGGGGATAT

**FIG. 4-3**

3951 GTTACAGAAC AAGGAAAACA GAACATAATA AAGTTAGAAG AGACAACCAA  
 4001 TCAAAAGGCT GAATTAATGG CTGTATTAAT AGCCTTGCAG GATTCCAAGG  
 4051 AGCAAGTAAA CATAGTAACA GACTCACAAT ATGTATTGGG CATCATATCC  
 4101 TCCCAACCAA CACAGAGTGA CTCCCCTATA GTTCAGCAGA TAATAGAGGA  
 4151 ACTAACAAAA AAGGAACGAG TGTATCTTAC ATGGGTTCCT GCTCACAAAG  
 4201 GCATAGGAGG AAATGAAAAA ATAGATAAAT TAGTAAGCAA AGACATTAGA  
 4251 AGAGTCCTGT TCCTGGAAGG AATAGATCAG GCACAAGAAG ATCATGAAAA  
 4301 ATATCATAGT AATTGGAGAG CATTAGCTAG TGACTIONTGGGA TTACCACCAA  
 4351 TAGTAGCCAA GGAAATCATT GCTAGTTGTC CTAAATGCCA TATAAAAGGG  
 4401 GAAGCAACGC ATGGTCAAGT AGACTACAGC CCAGAGATAT GGCAAATGGA  
 4451 TTGTACACAT TTAGAAGGCA AAATCATAAT AGTTGCTGTC CATGTAGCAA  
 4501 GTGACTTTAT AGAAGCAGAG GTGATACCAG CAGAAACAGG ACAGGAAACT  
 4551 GCCTATTTCC TGTAAAAATT AGCAGCAAGA TGGCCTGTCA AAGTAATACA  
 4601 TACAGACAAT GGACCTAATT TTACAAGTGC AGCCATGAAA GCTGCATGTT  
 4651 GGTGGACAGG CATAACAACAT GAGTTTGGGA TACCATATAA TCCACAAAGT  
 4701 CAAGGAGTAG TAGAAGCCAT GAATAAAGAA TTAAAATCTA TTATACAGCA  
 4751 GGTGAGGGAC CAAGCAGAGC ATTTAAAAAC AGCAGTACAA ATGGCAGTCT  
 4801 TTGTTCACAA TTTTAAAAGA AAAGGGGGGA TTGGGGGGTA CACTGCAGGG  
 4851 GAGAGACTAA TAGACATACT AGCATCACAA ATACAAACAA CAGAACTACA  
 4901 AAAACAAATT TTAAAAATCA ACAATTTTCG GGTCTATTAC AGAGATAGCA  
 4951 GAGACCCTAT TTGGAAAGGA CCGGCACAAC TCCTGTGGAA AGGTGAGGGG  
 5001 GCAGTAGTCA TACAAGATAA AGGAGACATT AAAGTGGTAC CAAGAAGAAA  
 5051 GGCAAAAATA ATCAGAGATT ATGGAAAACA GATGGCAGGT ACTGATAGTA  
 5101 TGGCAAATAG ACAGACAGAA AGTGAAAGCA TGGAACAGCC TGGTGAAATA  
 5151 CCATAAATAC ATGTCTAAGA AGGCCGCGAA CTGGCGTTAT AGGCATCATT  
 5201 ATGAATCCAG GAATCCAAAA GTCAGTTCGG CGGTGTATAT TCCAGTAGCA  
 5251 GAAGCTGATA TAGTGGTCAC CACATATTGG GGATTAATGC CAGGGGAAAG

**FIG. 4-4**



5301 AGAGGAACAC TTGGGACATG GGGTTAGTAT AGAATGGCAA TACAAGGAGT  
5351 ATAAACACA GATTGATCCT GAAACAGCAG ACAGGATGAT ACATCTGCAT  
5401 TATTTACAT GTTTTACAGA ATCAGCAATC AGGAAGGCCA TTCTAGGGCA  
5451 GAGAGTGCTG ACCAAGTGTG AATACCTGGC AGGACATAGT CAGGTAGGGA  
5501 CACTACAATT CTTAGCCTTG AAAGCAGTAG TGAAAGTAAA AAGAAATAAG  
5551 CCTCCCCTAC CCAGTGTCCA GAGATTAACA GAAGATAGAT GGAACAAGCC  
5601 CTGGAAAATC AGGGACCAGC TAGGGAGCCA TTCAATGAAT GGACACTAGA  
5651 GCTCCTGGAA GAGCTGAAAG AAGAAGCAGT AAGACATTTT CCTAGGCCTT  
5701 GGTTACAAGC CTGTGGGCAG TACATTTATG AGACTTATGG AGACACTTGG  
5751 GAAGGAGTTA TGGCAATTAT AAGAATCTTA CAACAACACT TGTTTACCCA  
5801 TTATAGAATT GGATGCCAAC ATAGTAGAAT AGGAATTCTC CCATCTAACA  
5851 CAAGAGGAAG AGGAAGAAGA AATGGATCCA GTAGATCCTG AGATGCCCCC  
5901 TTGGCATCAC CCTGGGAGCA AGCCCCAAC CCCTTGTAAT AATTGCTATT  
5951 GCAAAAGATG CTGCTATCAT TGCTATGTTT GTTTCACAAA GAAGGGTTTG  
6001 GGAATCTCCC ATGGCAGGAA GAAGCGAAGA AGACCAGCAG CTGCTGCAAG  
6051 CTATCCAGAT AATAAAGATC CTGTACCAGA GCAGTAAGTA ACGCTGATGC  
6101 ATCAAGAGAA CCTGCTAGCC TTAATAGCTT TAAGTGCTTT GTGTCTTATA  
6151 AATGTACTTA TATGGTTGTT TAACCTTAGA ATTTATTTAG TGCAAAGAAA  
6201 ACAAGATAGA AGGGAGCAGG AAATACTTGA AAGATTAAGG AGAATAAAGG  
6251 AAATCAGGGA TGACAGTGAC TATGAAAGTA ATGAAGAAGA ACAACAGGAA  
6301 GTCATGGAGC TTATACATAG CCATGGCTTT GCTAATCCCA TGTTTGAGTT  
6351 ATAGTAAACA ATTGATATGCC ACAGTTTATT CTGGGGTACC TGTATGGGAA  
6401 GAGGCAGCAC CAGTACTATT CTGTGCTTCA GATGCTAACC TAACAAGCAC  
6451 TGAACAGCAT AATATTTGGG CATCACAAGC CTGCGTTCCT ACAGATCCCA  
6501 ATCCACATGA ATTTCCACTA GGCAATGTGA CAGATAACTT TGATATATGG  
6551 AAAAATTACA TGGTGGACCA AATGCATGAA GACATCATTG GTTTGTGGGA  
6601 ACAGAGTTTA AAGCCTTGTG AGAAAATGAC TTTCTTATGT GTACAAATGA

**FIG. 4-5**

6651 ACTGTGTAGA TCTGCAAACA AATAAACAG GCCTATTAAA TGAGACAATA  
 6701 AATGAGATGA GAAATTGTAG TTTTAATGTA ACTACAGTCC TCACAGACAA  
 6751 AAAGGAGCAA AAACAGGCTC TATTCTATGT ATCAGATCTG AGTAAGGTTA  
 6801 ATGACTCAAA TGCAGTAAAT GGAACAACAT ATATGTTAAC TAATTGTAAC  
 6851 TCCACAATTA TCAAGCAGGC CTGTCCGAAG GTAAGTTTGT AGCCCATTCC  
 6901 CATACTAT TGTGCTCCAA CAGGATATGC CATCTTTAAG TGTAATGACA  
 6951 CAGACTTTAA TGGAACAGGC CTATGCCACA ATATTTTCAGT GGTTACTTGT  
 7001 ACACATGGCA TCAAGCCAAC AGTAAGTACT CAACTAATAC TGAATGGGAC  
 7051 ACTCTCTAGA GAAAAGATAA GAATTATGGG AAAAAATATT ACAGAATCAG  
 7101 CAAAGAATAT CATAGTAACC CTAAACACTC CTATAACAT GACCTGCATA  
 7151 AGAGAAGGAA TTGCAGAGGT ACAAGATATA TATACAGGTC CAATGAGATG  
 7201 GCGCAGTATG ACACTTAAAA GAAGTAACAA TACATCACCA AGATCAAGGG  
 7251 TAGCTTATTG TACATATAAT AAGACTGTAT GGGAAAATGC CCTACAACAA  
 7301 ACAGCTATAA GGTATTTAAA TCTTGTAAC CAAACAGAGA ATGTTACCAT  
 7351 AATATTCAGC AGAACTAGTG GTGGAGATGC AGAAGTAAGC CATTTACATT  
 7401 TTAAGTGTCA TGGAGAATTC TTTTATTGTA ACACATCTGG GATGTTTAAC  
 7451 TATACTTTTA TCAACTGTAC AAAGTCCGGA TGCCAGGAGA TCAAAGGGAG  
 7501 CAATGAGACC AATAAAAATG GTACTATACC TTGCAAGTTA AGACAGCTAG  
 7551 TAAGATCATG GATGAAGGGA GAGTCGAGAA TCTATGCACC TCCCATCCCC  
 7601 GGCAACTTAA CATGTCATTC CAACATAACT GGAATGATTC TACAGTTAGA  
 7651 TCAACCATGG AATTCCACAG GTGAAAATAC ACTTAGACCA GTAGGGGGAG  
 7701 ATATGAAAGA TATATGGAGA ACTAAATTGT ACAACTACAA AGTAGTACAG  
 7751 ATAAAACCTT TTAGTGTAGC ACCTACAAAA ATGTCAAGAC CAATAATAAA  
 7801 CATTACACC CCTCACAGGG AAAAAAGAGC AGTAGGATTG GGAATGCTAT  
 7851 TCTTGGGGGT GCTAAGTGCA GCAGGTAGCA CTATGGGCGC AGCGGCAACA  
 7901 GCGCTGACGG TACGGACCCA CAGTGTACTG AAGGGTATAG TGCAACAGCA  
 7951 GGACAACCTG CTGAGAGCGA TACAGGCCCA GCAACACTTG CTGAGGTTAT

**FIG. 4-6**

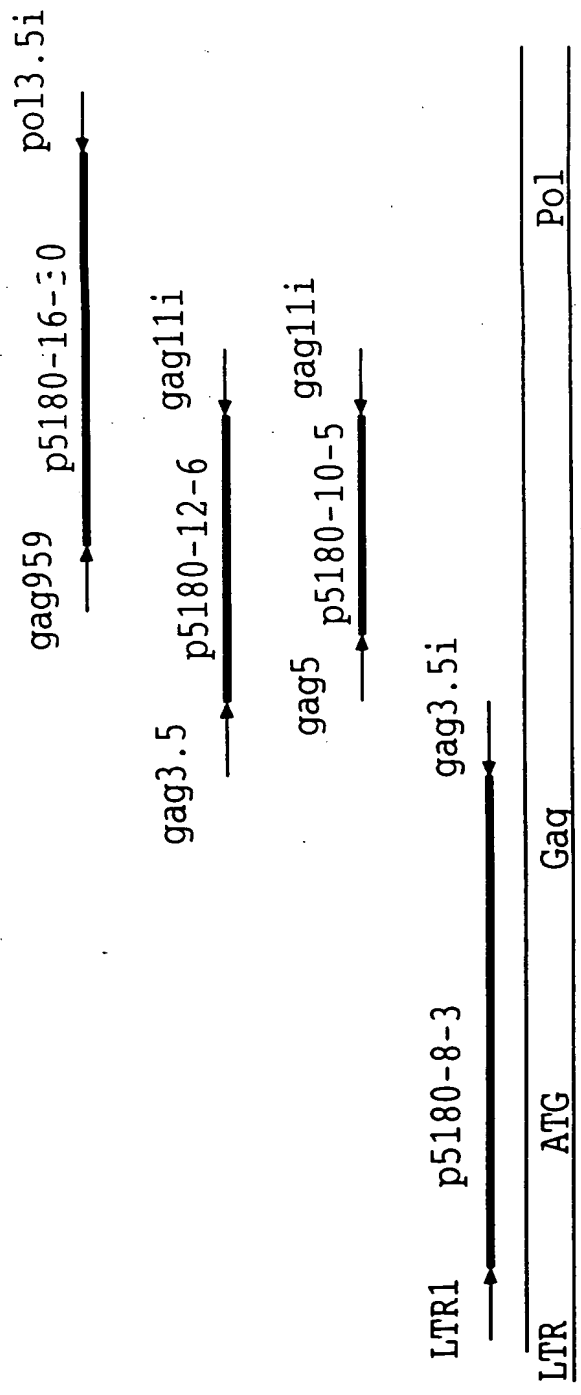
8001 CTGTATGGGG TATTAGACAA CTCCGAGCTC GCCTGCAAGC CTTAGAAACC  
 8051 CTTATACAGA ATCAGCAACG CCTAAACCTA TGGGGCTGTA AAGGAAAACT  
 8101 AATCTGTTAC ACATCAGTAA AATGGAACAC ATCATGGTCA GGAAGATATA  
 8151 ATGATGACAG TATTTGGGAC AACCTTACAT GGCAGCAATG GGACCAACAC  
 8201 ATAAACAATG TAAGCTCCAT TATATATGAT GAAATACAAG CAGCACAAGA  
 8251 CCAACAGGAA AAGAATGTAA AAGCATTGTT GGAGCTAGAT GAATGGGCCT  
 8301 CTCTTTGGAA TTGGTTTGAC ATA ACTAAAT GGTGTGGTA TATAAAAATA  
 8351 GCTATAATCA TAGTGGGAGC ACTAATAGGT ATAAGAGTTA TTATGATAAT  
 8401 ACTTAATCTA GTGAAGAACA TTAGGCAGGG ATATCAACCC CTCTCGTTGC  
 8451 AGATCCCTGT CCCACACCGG CAGGAAGCAG AAACGCCAGG AAGAACAGGA  
 8501 GAAGAAGGTG GAGAAGGAGA CAGGCCCAAG TGGACAGCCT TGCCACCAGG  
 8551 ATTCTTGCAA CAGTTGTACA CGGATCTCAG GACAATAATC TTGTGGACTT  
 8601 ACCACCTCTT GAGCAACTTA ATATCAGGGA TCCGGAGGCT GATCGACTAC  
 8651 CTGGGACTGG GACTGTGGAT CCTGGGACAA AAGACAATTG AAGCTTGTAG  
 8701 ACTTTGTGGA GCTGTAATGC AATATTGGCT ACAAGAATTG AAAAATAGTG  
 8751 CTACAAACCT GCTTGATACT ATTGCAGTGT CAGTTGCCAA TTGGACTGAC  
 8801 GGCATCATCT TAGGTCTACA AAGAATAGGA CAAGGATTCC TTCACATCCC  
 8851 AAGAAGAATT AGACAAGGTG CAGAAAGAAT CTTAGTGTA CATGGGGAAT  
 8901 GCATGGAGCA AAAGCAAATT TGCAGGATGG TCAGAAGTAA GAGATAGAAT  
 8951 GAGACGATCC TCCTCTGATC CTCAACAACC ATGTGCACCT GGAGTAGGAG  
 9001 CTGTCTCCAG GGAGTTAGCA ACTAGAGGGG GAATATCAAG TTCCCACACT  
 9051 CCTCAAACA ATGCAGCCCT TGCATTCTTA GACAGCCACA AAGATGAGGA  
 9101 TGTAGGCTTC CCAGTAAGAC CTCAAGTGCC TCTAAGGCCA ATGACCTTTA  
 9151 AAGCAGCCTT TGACCTCAGC TTCTTTTAA AAGAAAAGGG AGGACTGGAT  
 9201 GGGTTAATTT ACTCCCATAA GAGAGCAGAA ATCCTGGATC TCTGGATATA  
 9251 TCACACTCAG GGATTCTTCC CTGATTGGCA GTGTTACACA CCGGGACCAG  
 9301 GACCTAGATT CCCACTGACA TTTGGATGGT TGTTTAAACT GGTACCAGTG

**FIG. 4-7**

9351 TCAGCAGAAG AGGCAGAGAG ACTGGGTAAT ACAAATGAAG ATGCTAGTCT  
9401 TCTACATCCA GCTTGTAATC ATGGAGCTGA GGATGCACAC GGGGAGATAC  
9451 TAAAATGGCA GTTTGATAGA TCATTAGGCT TAACACATAT AGCCCTGCAA  
9501 AAGCACCCAG AGCTCTTCCC CAAGTAACTG ACACTGCGGG ACTTTCCAGA  
9551 CTGCTGACAC TGCGGGGACT TTCCAGCGTG GGAGGGATAA GGGGCGGTTC  
9601 GGGGAGTGGC TAACCCTCAG ATGCTGCATA TAAGCAGCTG CTTTCCGCTT  
9651 GTACCGGGTC TTAGTTAGAG GACCAGGTCT GAGCCCGGGA GCTCCCTGGC  
9701 CTCTAGCTGA ACCCGCTGCT TAACGCTCAA TAAAGCTTGC CTTGAGTGAG  
9751 AAGCAGTGTG TGCTCATCTG TTCAACCCTG GTGTCTAGAG ATC

**FIG. 4-8**

STRATEGY FOR PCR AMPLIFICATION,  
CLONING AND SEQUENCING:



**FIG. 5**

(SEQUENCE ID NO. 57 + 58)

MvP5180

|      |  |      |
|------|--|------|
| 685  | AAACCTCCGACGCAACGGGCTCGGCTTAGCGGAGTGCACCTGCTAAGAGG   | 734  |
| 1    | aaacctccaacgcaacgggctcggcttagcggagtgcacctgctaagagg   | 50   |
| 735  | CGAGAGGAACTCACAAGAGGGTGAGTAAATTTGCTGGCGGTGGCCAGACC   | 784  |
| 51   | cgagaggaactcacaagaggggtgagtaaatttgctggcgggtggccagacc | 100  |
| 785  | TAGGGGAAGGGCGAAGTCCCTAGGGGAGGAAGATGGGTGCGAGAGCGTCT   | 834  |
| 101  | taggggaagggcgaagtccctaggggaggaagatgggtgcgagacggtct   | 150  |
| 835  | GTGTTGACAGGGAGTAAATTGGATGCATGGGAACGAATTAGGTAAAGGCC   | 884  |
| 151  | gtgttgacagggagtaaattggatgcatgggaacgaattaggttaaggcc   | 200  |
| 885  | AGGATCTAAAAGGCATATAGGCTAAAACATTTAGTATGGGCAAGCAGGG    | 934  |
| 201  | aggatctaaaaaggcatataggctaaaAcatttagtatgggcaagcaggg   | 200  |
| 935  | AGCTGGAAAGATACGCATGTAATCCTGGTCTATTAGAAACTGCAGAAGGT   | 984  |
| 251  | agctggaaagatacgcatataatcctggtctactagaaactgcagaaggt   | 300  |
| 985  | ACTGAGCAA CTGCTACAGCAGTTAGAGCCAGCTCTCAAGACAGGGTCAGA  | 1034 |
| 301  | actgaacaactgctacagcagttagagccagctctcaagacagggtcaga   | 350  |
| 1035 | GGACCTGAAATCTCTCTGGAACGCAATAGCAGTACTCTGGTGC GTTCACA  | 1084 |
| 351  | ggacctgaaatccctctggaacgcaatagcagtactctggtgcgttcaca   | 400  |
| 1085 | ACAGATTTGACATCCGAGATACACAGCAGGCAATACAAAAGTTAAAGGAA   | 1134 |
| 401  | acagatttgacatccgagatacacagcaggcaatacaaaagttaaaggaa   | 450  |
| 1135 | GTAATGGCAAGCAGGAAGTCTGCAGAGGCCGCTAAGGAAGAAACAAGCCC   | 1184 |
| 451  | gtaatggcaagcaggaagtctgcagaggccgctaaggaagaaacaagctc   | 500  |

**FIG.6-1**



|      |   |      |
|------|---|------|
| 1685 | AACCATTTCAGAGATTATGTAGATCGGTTTTACAAAACATTAAGAGCTGAG     | 1734 |
| 1001 | <br>aaccatttcagagattatgtagatcggttttacaaaacattaagagctgag | 1050 |
| 1735 | CAAGCTACTCAAGAAGTAAAGAATTGGATGACAGAAACCTTGCTTGTTCA      | 1784 |
| 1051 | <br>caagctactcaagaagtaaagaattggatgacagaaaccctcgttgttca  | 1100 |
| 1785 | GAATTCAAACCCAGATTGTAAACAAATTCTGAAAGCATTAGGACCAGAAG      | 1834 |
| 1101 | <br>gaattcaaaccagattgtaaacaattctgaaagcattaggaccaggag    | 1150 |
| 1835 | CTACTTTAGAAAGAAATGATGGTAGCCTGTCAAGGAGTAGGAGGGCCAAC      | 1884 |
| 1151 | <br>ctactttagaagaaatgatggtagcctgtcaaggagtaggagggccaact  | 1200 |
| 1885 | CACAAGGCAAAAATACTAGCAGAAGCAATGGCTTCTGCCCAGCAAGATTT      | 1934 |
| 1201 | <br>cacaaggcaaaaatactagcagaagcaatggcttctgcccagcaagattt  | 1250 |
| 1935 | AAAAGGAGGATACACAGCAGTATTCATGCAAGAGGGCAGAATCCAAATA       | 1984 |
| 1251 | <br>aaaggaggatacacagcagtattcatgcaagagggcagaatccaaata    | 1300 |
| 1985 | GAAAAGGGCCCATAAATGCTTCAATTGTGGAAGAGGGACATATAGCA         | 2034 |
| 1301 | <br>gaaaagggcctataaaatgtttcaattgtggaaaagagggacatatagca  | 1350 |
| 2035 | AAAACTGTGCGAGCACCTAGAAAAAGGGGTTGCTGGAAATGTGGACAGGA      | 2084 |
| 1351 | <br>aaaaactgtcgagcacctagaagaaggggttactggaaatgtggacagga  | 1400 |
| 2085 | AGGTCACCAAAATGAAAGATTGCAAAAATGGAAGACAGGCAAATTTTTTAG     | 2134 |
| 1401 | <br>aggtcaccaaatgaaagattgcaaaaatggaagacaggctaatttttttag | 1450 |
| 2135 | GGAAGTACTGGCCTCCGGGGGGCACGAGGCCAGGCAATTATGTGCAGAAA      | 2184 |
| 1451 | <br>ggaagtactggcctccggggggcacgaggccagccaattatgtgcagaaa  | 1500 |

**FIG. 6-3**



|      |  |                     |
|------|--|---------------------|
| 2185 | CAAGTGTCCCCATCAGCCCCACCAATGGAGGAGGCAGTGAAGGAACAAGA | 2234                |
| 1501 | caagtgtccccatcagccccaccaatggaggaggcagtgaaggaacaaga | 1550                |
| 2235 | GAATCAGAGTCAGAAGGGGGATCAGGAAGAGCTGTACCCATTTGCCTCCC | 2284                |
| 1551 | gaatcagaatcaaaagggggatcaggaagagctgtacccatttgcctccc | 1600                |
| 2285 | TCAAATCCCTCTTTGGGACAGACCAATAGTCACAGCAAAGGTTGGGGGTC | 2334                |
| 1601 | tcaaatccctctttgggacagaccaatagtcacagcaaaggttgggggcc | 1650                |
| 2335 | ATCTATGTGAGGCTTTACTGGATACAGGGGCAGATGATACAGTATTAAAT | 2384                |
| 1651 | atctatgtgaggctttactggatacaggggcagatgatacagtattaaat | 1700                |
| 2385 | AACATACAATTAGAAGGAAGATGGACACCAAAA                  | 2417 (SEQ ID NO:57) |
| 1701 | aacatacaattagaaggaagatggacacccaaa                  | 1733 (SEQ ID NO:58) |

**FIG. 6-4**

MVP5180 MGARASVLTGSKLDAWERIRLRPGSKKAYRLKHLVWASRELERYACNPGL  
PCR MGARRSVLTGSKLDAWERIRLRPGSKKAYRLKHLVWASRELERYAYNPGL

LETAEGTEQLLOQLEPALKTGSEDLKSLWNAIAVLWCVHNRFDIRDTQQA  
LETAEGTEQLLOQLEPALKTGSEDLKSLWNAIAVLWCVHNRFDIRDTQQA

IQKLKEVMASRKSAEAAKEETSPROTSONYPIVTNAOGOMVHOAISPRTL  
IQKLKEVMASRKSAEAAKEETSSTQASQNYPIVTNAOGOMVHOAISPRTL

NAWVKAVEEKAFNPEIIPMFALSEGAVPYDINTMLNAIGGHQALQVLK  
NAWVKAVEEKAFNPEIIPMFALSEGAVPYDINTMLNAIGGHQALQVLK

EVINEEAAEWDRTHTPPAMGPLPPGOIREPTGSDIAGTTSTQOEQI IWTR  
EVINEEADWDRTHTPPAMGPLPPGOIREPTGSDIAGTTSTQOEQI IWTR

GANSIPVGDIYRKWIVLGLNKMVKMYSVPSILDIRQGPKEPFRDYVDRFY  
GANSIPVGDIYRKWIVLGLNKMVKMYSVPSILDIRQGPKEPFRDYVDRFY

KTLRAEQATQEVKNWMTETLLVONSNPDCKQILKALGPEATLEEMMVACQ  
KTLRAEQATQEVKNWMTETLVVQNSNPDCQILKALGPGATLEEMMVACQ

GVGGPTHKAKILAEAMASAQQDLKGGYTAVFMORGONPNRKGPIKCFNCG  
GVGGPTHKAKILAEAMASAQQDLKGGYTAVFMORGONPNRKGPIKCFNCG

KEGHIAKNCRAPRKRCWKCGQEGHOMKDCKNGRQANFLGKYWPPGGTRP  
KEGHIAKNCRAPRRRGYWKCGQEGHOMKDCKNGRQANFLGKYWPPGGTRP

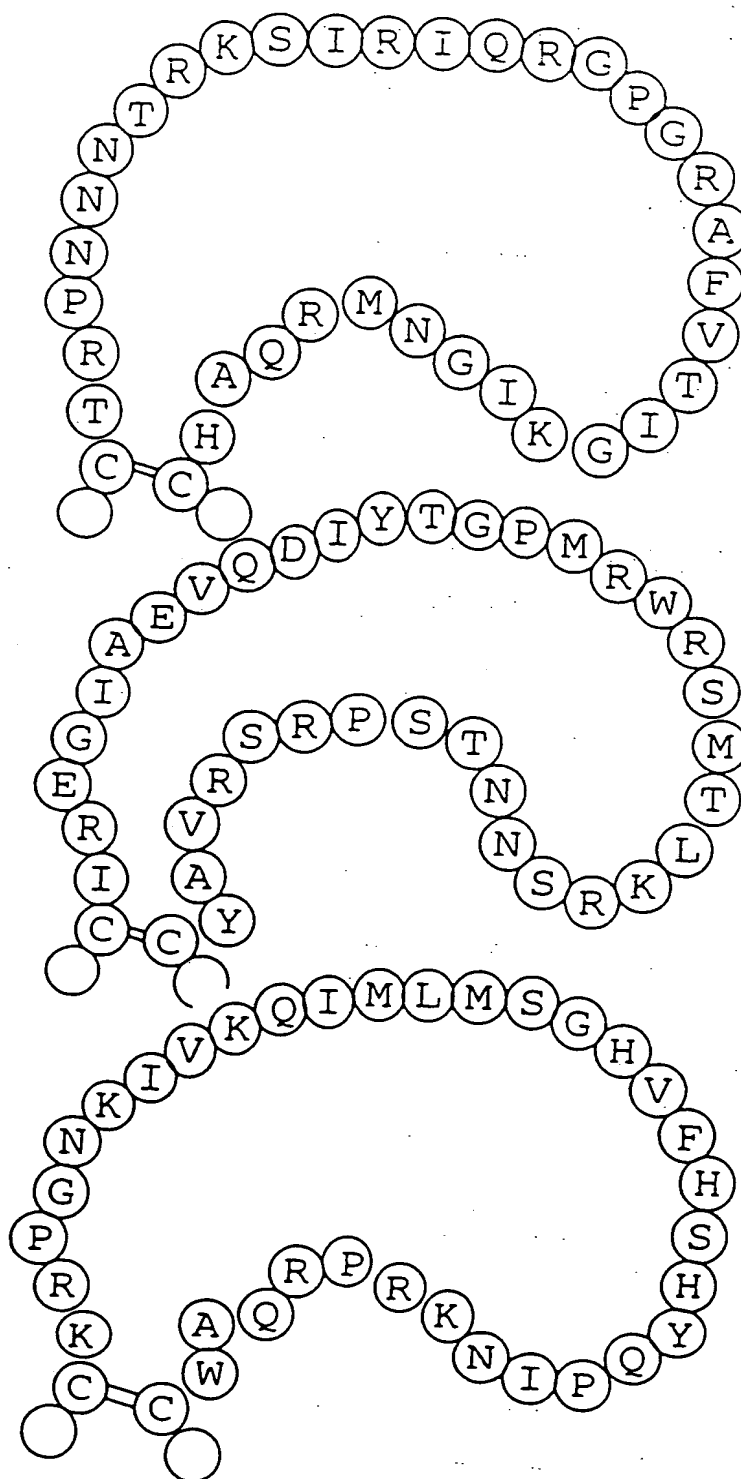
GNYVQKQVSPSAPPMEEAVKEQENQSKGDOEELYPFASLSLFGTDQ (SEQ ID NO:59)  
ANYVQKQVSPSAPPMEEAVKEQENQKQKGDQEELYPFASLSLFGTDQ (SEQ ID NO:60)

**FIG. 7**

HIV - 1 (LAI)  
(SEQ ID NO:66)

HIV - 5180  
(SEQ ID NO:54)

HIV - 2 (ROD)  
(SEQ ID NO:67)



**FIG. 8**